

REMARKS

Claims 1-3, 48, and 57 have been amended and claim 59 has been added. Claims 9, 12-45, 49-54, and 56 have been canceled without prejudice or disclaimer. Claims 1-8, 10, 11, 48, 55, and 57-59 are pending in the instant application. Support for the amendments to the claims can be found in the specification at, for example, page 32 (Table I), page 35, lines 21-27, and in Figures 1-7 and 9. No new matter has been added as a result of the above-described amendments. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

1. Rejections of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph

The Office Action asserts a rejection of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Action states that because one of ordinary skill in the art cannot envision the detailed structure of a genus of polynucleotide variants comprising allelic or splice variants of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; sequences that are at least 70% identical to SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; or sequences that hybridize under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, the specification does not meet the written description requirement for claiming such genera. Specifically, the Action states that because these genera are highly variant, the species disclosed in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 are not representative of these genera.

Applicants have amended claim 1 to recite an isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; a nucleotide sequence encoding a polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6; or a nucleotide sequence that is complementary to the nucleotide sequence of either of these nucleic acid molecules.

Applicants contend that because claim 1, as amended, no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of

the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, amended claim 1 satisfies the requirements of 35 U.S.C. § 112, first paragraph.

Applicants have amended claim 2 to recite an isolated nucleic acid molecule comprising a region of the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5 encoding a polypeptide fragment of at least 25 amino acid residues, wherein the polypeptide fragment has an activity of a polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, or is antigenic; a region of the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5 comprising a fragment of at least 16 nucleotides; or a nucleotide sequence that is complementary to the nucleotide sequence of either of these nucleic acid molecules. Applicants contend that because claim 2, as amended, no longer recites allelic or splice variants of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; sequences that are at least 70% identical to SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; or sequences that hybridize under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, amended claim 2 satisfies the requirements of 35 U.S.C. § 112, first paragraph.

Applicants have similarly amended claim 3 so that it no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants, therefore, respectfully contend that amended claim 3 also satisfies the requirements of 35 U.S.C. § 112, first paragraph.

In addition, Applicants wish to direct the Examiner's attention to new claim 59, which has been added to more particularly point out and distinctly claim the subject matter that Applicants regard as the invention. The amino acid sequence recited in claim 59 is based on an amino acid sequence comparison of several murine and human B7-like polypeptides that indicates the structural features shared by these sequences (Appendix A). Applicants contend that the instant specification teaches one of ordinary skill in the art to perform a sequence comparison of the murine and human B7-like polypeptides disclosed in the instant specification in order to determine the positions within the human B7-like polypeptide sequence where substitutions, either conservative or nonconservative, would be tolerated, and that such a comparison was well within the skill of one having ordinary skill

in the art. Support for claim 59 can be found in the specification at, for example, page 32 (Table I), page 35, lines 21-27, and in Figures 1-7 and 9.

The Office Action also asserts a rejection of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph, because the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with the claims.

The Action first asserts that because the specification does not provide sufficient guidance (*e.g.*, a functional assay) or evidence regarding B7-like activity, one of ordinary skill in the art could not reasonably determine whether any of the nucleic acid molecules encompassed by claims 1-3 encodes a polypeptide having B7-like activity, and therefore, would require undue experimentation to use the claimed nucleic acid molecules. The Action also asserts that because the specification does not provide sufficient guidance or evidence regarding the residues of B7-like polypeptide that are essential for B7-like activity, and because even a single amino acid substitution can have an unpredictable effect on polypeptide activity, one of ordinary skill in the art would require undue experimentation to identify polypeptides having B7-like activity, and therefore, would require undue experimentation to make the nucleic acid molecules encoding such polypeptides.

Applicants respectfully disagree with the Action's assertion that one of ordinary skill in the art could not reasonably determine whether any of the nucleic acid molecules encompassed by claims 1-3 encodes a polypeptide having B7-like activity. Applicants wish to direct the Examiner's attention to page 93, lines 7-9 of the specification, where Applicants teach that transgenic mice expressing a B7-like polypeptide exhibit seminal vesicle hyperplasia. Applicants, therefore, respectfully contend that in view of the specification's teachings, one of ordinary skill in the art could readily determine whether a specific nucleic acid molecule encodes a polypeptide having B7-like activity by expressing the molecule in a mouse and determining whether the mouse exhibits seminal vesicle hyperplasia. Applicants also disagree with the Action's assertion that the specification does not provide sufficient teaching regarding the residues of B7-like polypeptide that are essential for B7-like activity. As discussed above, Applicants contend that the specification teaches one of ordinary skill in the art to perform a sequence comparison of B7-like polypeptide orthologs in order to determine the positions within the human B7-like polypeptide sequence where amino acid substitutions are tolerated, and that such a comparison was well within the skill of one

having ordinary skill in the art. Applicants, therefore, respectfully contend that claims 1-3 fulfill the requirements of 35 U.S.C. § 112, first paragraph.

The Action next asserts that because gene therapy was unpredictable at the time the instant application was filed, and because the specification does not provide sufficient guidance or evidence correlating the modulation of B7-like polypeptide levels in an animal with a therapeutic effect in that animal, one of ordinary skill in the art would require undue experimentation to use the method of claim 55. The Action also asserts that because the term "modulating" encompasses increasing or decreasing the level B7-like polypeptides in an animal, and the specification does not provide sufficient guidance or evidence as to how the claimed nucleic acid molecules can be used to decrease B7-like polypeptide levels in an animal, one of ordinary skill in the art would require undue experimentation to use the method of claim 55.

Applicants respectfully disagree with the Action's assertion, and contend that one with skill in the art could readily practice the claimed method using, for example, B7-like antisense inhibitors or dominant negative mutants identified by the genetic suppressor element (GSE) screening approach disclosed in U.S. Patent Nos. 5,217,889 and 5,811,234 (to Roninson *et al.*). Applicants contend that nucleic acid molecules encoding dominant negative mutants could be used to decrease B7-like polypeptide levels in an animal. Applicants, therefore, respectfully request that this rejection be withdrawn.

The Action next asserts that while the specification is enabling for nucleotide sequences that hybridize under moderately or highly stringent conditions to the "full complement" of a nucleotide sequence encoding a polypeptide having B7-like activity, the specification is not enabling for nucleotide sequences that hybridize under moderately or highly stringent conditions to the "complement" of a nucleotide sequence encoding a polypeptide having B7-like activity. Specifically, the Action asserts that by using the term "complement," rather than the term "full complement," the nucleic acid molecules of claims 1(c), 2(e), and 3(g) read on any nucleic acid molecule comprising one or more nucleotides, including nucleic acid molecules that do not encode polypeptides possessing B7-like activity.

Applicants respectfully disagree with the Action's assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Applicants contend that such a

meaning is contrary to the established meaning of the term "nucleotide sequence complement" in the art. For example, Alberts *et al.* describes a complementary sequence as "a mold of the original," such that the sequence of nucleotides in a nucleic acid molecule is *preserved* in its complementary strand. Alberts *et al.*, *Molecular Biology of the Cell*, pp. 5-7 (Garland Publishing, Inc., 1994). Applicants, therefore, contend that the nucleotide sequence complement of the nucleotide sequence 5'-A-G-C-T-A-G-C-T-3' is well understood in the art to be 5'-T-C-G-A-T-C-G-A-3', and not one or more nucleotides of that nucleic acid molecule. Nevertheless, Applicants have amended claims 1-3, as described above, so that these claims no longer recite an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants, therefore, respectfully contend that claims 1-3, as amended, fulfill the requirements of 35 U.S.C. § 112, first paragraph.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, first paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

2. Rejections of claims 1-3, 8, 10, and 55 under 35 U.S.C. § 112, second paragraph

The Office Action asserts a rejection of claims 1-3, 8, 10, and 55 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention.

The Action first asserts that claims 8, 10, and 55 are indefinite for reciting the term "B7-like polypeptide." Applicants are unclear as to the basis of this rejection, since the Action *both* states that the specification does not define the term (page 16, lines 5-7) *and* that the specification defines the term using only amino acid sequences (*i.e.*, as indicated by sequence identifiers) without identifying a function or biological activity for these amino acid sequences (page 16, lines 7-9). However, in order to provide a reply to the instant Office Action that is fully responsive, Applicants address each of the Action's assertions.

With regard to the Action's assertion that the specification does not define the term "B7-like polypeptide," Applicants wish to direct the Examiner's attention to page 16, lines 23-28 of the specification, where the term is clearly defined as referring to "one or more recombinant human

polypeptides comprising the amino acid sequence of SEQ ID NOs: 2, 4, 6 or 8, related polypeptides thereto, or recombinant murine polypeptides comprising the amino acid sequence of SEQ ID NOs: 10, 11 or 12, and related polypeptides thereto." The specification also defines "related polypeptides" at page 16, lines 29-32 as including "B7-like polypeptide allelic variants, B7-like polypeptide orthologs, B7-like polypeptide splice variants, B7-like polypeptide variants and B7-like polypeptide derivatives." The specification further defines "B7-like polypeptide allelic variants," "B7-like polypeptide orthologs," "B7-like polypeptide splice variants," "B7-like polypeptide variants," and "B7-like polypeptide derivatives," at page 17, lines 4-8; page 18, lines 20-25; page 18, lines 26-31; page 18, line 32 to page 19, line 7; and page 17, lines 9-15, respectively. As the specification clearly defines the term "B7-like polypeptide," Applicants contend that claims 8, 10, and 55 are *not* indefinite for reciting this term and respectfully request withdrawal of this ground of rejection.

Applicants next address the Action's assertion that the specification defines the term "B7-like polypeptide" using only amino acid sequences without identifying a function or biological activity for these amino acid sequences. Applicants note that in light of the specification's teachings (as discussed above), the term "B7-like polypeptide" describes a class of molecules comprising polypeptides having a particular amino acid sequence (*e.g.*, the amino acid sequence of SEQ ID NO: 2) and related polypeptides having similar amino acid sequences. Applicants contend that because the term "B7-like polypeptide" describes a class of molecules using a characteristic property of that class (*i.e.*, amino acid sequence), the recitation of this term in the claims does not render those claims indefinite. Applicants therefore, respectfully request withdrawal of this ground of rejection.

The Action next asserts that there is insufficient antecedent basis in claims 1-3 for the phrase "the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants respectfully contend that because claims 1-3 have been amended as suggested in the Action to recite "a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6," this ground of rejection should be withdrawn.

The Action next asserts that there is insufficient antecedent basis in claims 1-3 for the phrase "the encoded polypeptide." Applicants respectfully disagree with the Action's assertion, and contend that the antecedent basis for the phrase "the encoded polypeptide" in, for example, line 4 of claim 3, is the phrase "a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 with at least one conservative amino acid substitution," in lines 2-3. In other words, "the encoded

polypeptide” of claim 3(a) is the “polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 with at least one conservative amino acid substitution” that is encoded by the nucleotide sequence of that subpart.

The Action next asserts that claims 48 and 57 are indefinite for reciting the phrase “a nucleic acid molecule of any of Claims 1, 2, or 3,” because the phrase does not particularly point out which molecule “a nucleic acid molecule” refers to in the claim. Applicants respectfully contend that because claims 48 and 57 have been amended as suggested in the Action to recite “the nucleic acid molecule of any of Claims 1, 2, or 3,” this ground of rejection should be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, second paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

3 . Rejections of claims 1-3 under 35 U.S.C. § 102

The Office Action asserts a rejection of claims 1-3 under 35 U.S.C. § 102(a), as being anticipated by Marra *et al.* (The Washington University-NCI Mouse EST project, seq_name: gb_est82:BF040046, July 2, 1999; GenBank Accession No. AI790785), contending that Marra *et al.* disclose an EST sequence that shares 85% similarity with the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5. The Action states that the sequence disclosed by Marra *et al.* reads on a “sequence that is complementary to any of the claimed sequences,” since “[a] sequence that is complementary would encompass a nucleotide with one base pair or more in common with any claimed sequence.” The Action also states that because of the breadth of the phrase “an activity of the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6,” which encompasses any activity – including antigenicity, Marra *et al.* anticipates claims 1-3, since the sequence disclosed by Marra *et al.* is antigenic when administered to an animal.

Marra *et al.* disclose a nucleotide sequence of 530 bp. SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 set forth nucleotide sequences of 1146 bp, 1158 bp, and 1158 bp, respectively. Exhibits A-C indicate that there is an overlap of no more than 274 bp or 286 bp between the nucleotide sequence disclosed by Marra *et al.* and the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5. Exhibits A-C also indicate that in the overlapping regions, the sequences share an identity of between 69.6% to 72.6%, and *not* 85% (Applicants understand the

Office Action to mean 85% *identity*, rather than *similarity*, since the term "similarity" refers to the degree of sequence relatedness between two polypeptide sequences, and is defined as such in the instant specification at page 21, lines 6-20).

As discussed above in section 1 above, Applicants respectfully disagree with the Action's assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Applicants contend that such a meaning is contrary to the established meaning of the term "nucleotide sequence complement" in the art. Applicants, therefore, contend that the sequence of Marra *et al.*, which is *less than half* the length of the sequences of SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5, and which shares an identity of between 69.6% and 72.6% with these sequences, *cannot* anticipate a nucleotide sequence that is complementary to the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5. Moreover, Applicants contend that since none of the pending claims reads upon *any* polypeptide having "an activity of the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6," it is *not* sufficient, for Marra *et al.* to anticipate claims 1-3, that the sequence disclosed by Marra *et al.* merely be antigenic when administered to an animal. Rather, for Marra *et al.* to anticipate claims 1-3, the sequence disclosed by Marra *et al.* must meet each and every limitation of the claimed invention. Because Marra *et al.* does not disclose a sequence that meets each and every limitation of the claimed invention, Marra *et al.* *cannot* anticipate claims 1-3. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Office Action also asserts a rejection of claims 1-3 under 35 U.S.C. § 102(b), as being anticipated by Taudien *et al.* (GenBank Accession No. AF121782, published February 2, 1999), contending that "Taudien *et al.* disclose a nucleotide sequence that is complementary to the nucleotide sequences from SEQ ID NO[s]: 1-6." The Action suggests that this rejection can be overcome by amending claims 1(d), 2(f), and 3(h) to replace the phrase "a nucleotide sequence complementary to the nucleotide sequence" with the phrase "a nucleotide sequence that is the full complement of the nucleotide sequence."

Taudian *et al.* disclose a *genomic* sequence of 142,742 nucleotides for human chromosome 21q22.3 PAC 206A10. SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 set forth *cDNA* sequences for human B7-like polypeptide. Exhibits D-F indicate that the open reading frames of the

cDNA sequences of SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 (*i.e.*, the 1149-1161 nucleotide sequences encoding the amino acid sequences of SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 6) share an identity of between only 62.2 and 62.5% with the genomic sequence disclosed of Taudian *et al.*

As discussed above, Applicants respectfully disagree with the Action's assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Because the genomic sequence of Taudian *et al.* shares an identity of between only 62.2 and 62.5% with the coding portion of the cDNA sequences of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5, Taudian *et al.* cannot anticipate claims directed to a nucleotide sequence that is complementary to the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 102 have been traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

CONCLUSIONS

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited.

If Examiner Whiteman believes it to be helpful, he is invited to contact the undersigned representative by telephone at (312) 913-0001.

Respectfully submitted,
McDonnell Boenhen Hulbert & Berghoff

Dated: April 2, 2003

By:

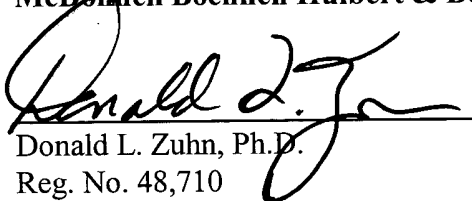

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EXHIBIT A

	10	20	30	40	50	60
	* *	* *	* *	* *	* *	* *
SEQ01_ORF	ATGGGGCTTG	TGATTTTCCT	CCACGGTTCT	GGGTCTGGTA	ATGAAGTCAT	AGAAGGCCCC
	TACCCCGAAC	ACTAAAAGGA	GGTGCCAAGA	CCCAGACCAT	TACTTCAGTA	TCTTCCGGGG
	260	270	280	290	300	310
Marra EST	cTGGTcaTcc	TGgcTcagCT	gacaGcTTCc	GGaTCcaGtT	ATcAgaTCAT	AGAAGGtCCt>
SEQ01_ORF	ATGGGGCTTG	TGATTTTCCT	CCACGGTTCT	GGGTCTGGTA	ATGAAGTCAT	AGAAGGCCCC
	70	80	90	100	110	120
	* *	* *	* *	* *	* *	* *
SEQ01_ORF	CAGAAATGCAA	CAGTCCTGAA	GGGCTCCCAG	GCTCGCTTCA	ACTGCACCGT	CTCCCAGGGC
	GTCTTACGTT	GTCCAGGACTT	CCCAGAGGTC	CGAGCGAAGT	TGACGTGGCA	GAGGGTCCCG
	320	330	340	350	360	370
Marra EST	CAGAAATGtAA	CAGTCCTaAA	GGaCTCagAG	GCTCaCTTCA	ACTGCACCGT	gaCtAcGGC>
SEQ01_ORF	CAGAAATGCAA	CAGTCCTGAA	GGGCTCCCAG	GCTCGCTTCA	ACTGCACCGT	CTCCCAGGGC
	130	140	150	160	170	180
	* *	* *	* *	* *	* *	* *
SEQ01_ORF	TGGAAGCTCA	TCATGTGGGC	TCTCAGTGAC	ATGGTGGTGC	TAAGCGTCAG	GCCCATGGAG
	ACCTTCGAGT	AGTACACCCG	AGAGTCACTG	TACCACCACG	ATTCGCAGTC	CGGGTACCTC
					a	
	380	390	400	410	420	430
Marra EST	TGGAAGCTtc	TCATGTGGaC	TCTtAaccAa	ATGGTGGTGC	TgAGtcTCcc	aCCCAaGG-a>
SEQ01_ORF	TGGAAGCTCA	TCATGTGGGC	TCTCAGTGAC	ATGGTGGTGC	TAAGCGTCAG	GCCCATGGAG
	190	200	210	220	230	240
	* *	* *	* *	* *	* *	* *
SEQ01_ORF	CCCATCATCA	CCAATGACCG	CTTCACCTCT	CAGAGGTACG	ACCAGGGCGG	GAACTTCACC
	GGGTAGTAGT	GGTTACTGGC	GAAGTGGAGA	GTCTCCATGC	TGGTCCC GCC	CTTGAAGTGG
					c	
	440	450	460	470	480	490
Marra EST	CCCATCATCA	CCAaCaACCG	tTTCACCTaT	gccAGtTA-c	AaCAGcatGa	cAgCTTCaTc>
SEQ01_ORF	CCCATCATCA	CCAATGACCG	CTTCACCTCT	CAGAGGTACG	ACCAGGGCGG	GAACTTCACC
	250	260	270	280	290	300
	* *	* *	* *	* *	* *	* *
SEQ01_ORF	TCGGAGATGA	TCATCCACAA	TGTGGAGCCC	AGTGATTTCGG	GGAACATCAG	ATGCAGCCTC
	AGCCTCTACT	AGTAGGTGTT	ACACCTCGGG	TCACTAAGCC	CCTTG TAGTC	TACGTCGGAG
	500	510	520			
Marra EST	TCGGAGtTGA	TCATCCaTgA	TGTGcAGCCC	AGTG>		
SEQ01_ORF	TCGGAGATGA	TCATCCACAA	TGTGGAGCCC	AGTG		

	310	320	330	340	350	360
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	CAGAACAGTC	GCCTGCATGG	ATCTGCTTAC	CTTACCGTCC	AAGTTATGGG	AGAGCTGTTC
	GTCTTGTCAG	CGGACGTACC	TAGACGAATG	GAATGGCAGG	TTCAATACCC	TCTCGACAAG
	370	380	390	400	410	420
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	ATTCCCAGTG	TTAATCTTGT	AGTCGCTGAG	AATGAACCTT	GTGAAGTTAC	TTGTCTACCC
	TAAGGGTCAC	AATTAGAACA	TCAGCGACTC	TTACTTGGAA	CACTTCAATG	AACAGATGGG
	430	440	450	460	470	480
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	TCACACTGGA	CCCGGCTCCC	GGATATTTCC	TGGGAGCTCG	GTCTCCTGGT	CAGCCATTCA
	AGTGTGACCT	GGGCCGAGGG	CCTATAAAGG	ACCCTCGAGC	CAGAGGACCA	GTCGGTAAGT
	490	500	510	520	530	540
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	AGCTATTATT	TTGTTCGGGA	GCCCAGCGAC	CTTCAAAGTG	CAGTGAGCAT	CCTGGCTCTG
	TCGATAATAA	AACAAGGCCT	CGGGTCGCTG	GAAGTTTCAC	GTCACTCGTA	GGACCGAGAC
	550	560	570	580	590	600
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	ACCCACAGAG	GCAATGGGAC	TTTGACTTGC	GTGGCTACCT	GGAAGAGCCT	GAAGGCCCGC
	TGGGGTGTCT	CGTTACCCTG	AAACTGAACG	CACCGATGGA	CCTTCTCGGA	CTTCCGGGCG
	610	620	630	640	650	660
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	AAGTCTGCAA	CTGTAAATCT	CACGTGTGATT	CGGTGTCCCC	AAGACACTGG	AGGTGGTATT
	TTCAGACGTT	GACATTTAGA	GTGACACTAA	GCCACAGGGG	TTCTGTGACC	TCCACCATAA
	670	680	690	700	710	720
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	AATATTCCAG	GTGTATTATC	AAGTTTACCG	AGTTTAGGTT	TTTCATTGCC	TACTTGGGGC
	TTATAAGGTC	CACATAATAG	TTCAAATGGC	TCAAATCCAA	AAAGTAACGG	ATGAACCCCG
	730	740	750	760	770	780
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	AAAGTTGGAC	TTGGACTAGC	AGGCACCATG	CTTCTGACGC	CGACGTGTAC	TCTTACAATA
	TTTCAACCTG	AACCTGATCG	TCCGTGGTAC	GAAGACTGCG	GCTGCACATG	AGAATGTTAT
	790	800	810	820	830	840
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	CGCTGCTGCT	GCTGCCGCCG	TCGTTGTTGT	GGCTGCAACT	GCTGCTGCCG	TTGTTGTTTC
	GCGACGACGA	CGACGGCGGC	AGCAACAACA	CCGACGTTGA	CGACGACGGC	AACAACAAAG
	850	860	870	880	890	900
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	TGCTGTAGAA	GAAAAAGAGG	ATTTCGTATT	CAATTTCAAA	AGAAATCTGA	AAAAGAGAAG
	ACGACATCTT	CTTTTCTCCT	TAAAGCATAA	GTTAAAGTTT	TCTTTAGACT	TTTTCTCTTC

	910	920	930	940	950	960
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	ACAAACAAAG	AAACTGAGAC	AGAAAGTGGA	AATGAAAAC	CCGGCTACAA	TTCAGATGAA
	TGTTTGTTC	TTTGACTCTG	TCTTTCACCT	TTACTTTTGA	GGCCGATGTT	AAGTCTACTT
	970	980	990	1000	1010	1020
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	CAAAAGACCA	CAGACACCGC	TTCTCTCCCT	CCCAAATCCT	GTGAATCCAG	TGATCCTGAA
	GTTTTCTGGT	GTCTGTGGCG	AAGAGAGGGA	GGGTTTAGGA	CACTTAGGTC	ACTAGGACTT
	1030	1040	1050	1060	1070	1080
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	CAAAGAAACA	GTAGCTGTGG	CCCTCCTCAC	CAGCGGGCTG	ATCAACGTCC	ACCCAGGCCA
	GTTTCTTTGT	CATCGACACC	GGGAGGAGTG	GTCGCCCAC	TAGTTGCAGG	TGGGTCCGGT
	1090	1100	1110	1120	1130	1140
	* * * *	* *	* *	* *	* *	* *
SEQ01_ORF	GCAAGTCATC	CACAGGCTTC	TTTAAATCTG	GCCAGTCCTG	AGAAGGTCAG	TAATACAAC
	CGTTCAGTAG	GTGTCCGAAG	AAAATTAGAC	CGGTCAGGAC	TCTTCCAGTC	ATTATGTTGA
	*					
SEQ01_ORF	GTAGTA					
	CATCAT					

EXHIBIT B

	10	20	30	40	50	60
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	ATGGTGGCAG	GAGCCATGGA	AAATAGAGAC	CCACCCGGTT	CTGGGTCTGG	TAATGAAGTC
	TACCACCGTC	CTCGGTACCT	TTTATCTCTG	GGTGGGCCAA	GACCCAGACC	ATTACTTCAG
	260	270	280	290	300	
Marra EST	gtTgCtG--gt	cAtC-cTG--	-gc-tcA-gC	tg-aCaGcTT	CcGGaTCcaG	TtATcAgaTC>
SEQ03_ORF	ATGGTGGCAG	GAGCCATGGA	AAATAGAGAC	CCACCCGGTT	CTGGGTCTGG	TAATGAAGTC
	70	80	90	100	110	120
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	ATAGAAGGCC	CCCAAAATGC	AAGAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC
	TATCTTCCGG	GGGTTTACG	TTCTCAGGAC	TTCCCAGAGG	TCCGAGCGAA	GTTGACGTGG
	310	320	330	340	350	360
Marra EST	ATAGAAGGtC	CtCAgAATGt	AAcAGTCCTa	AAGGaCTCag	AGGCTCaCTT	CAACTGCACC>
SEQ03_ORF	ATAGAAGGCC	CCCAAAATGC	AAGAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC
	130	140	150	160	170	180
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC
	CAGAGGGTCC	CGACCTTCGA	GTAGTACACC	CGAGAGTCAC	TGTACCACCA	CGATTTCGAG
						a
	370	380	390	400	410	420
Marra EST	GTGaCtCAcG	GCTGGAAGCT	tcTCATGTGG	aCTCTtAacc	AaATGGTGGT	GCTgAGtcTC>
SEQ03_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC
	190	200	210	220	230	240
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC
	TCCGGGTACC	TCGGGTAGTA	GTGGTTACTG	GCGAAGTGGA	GAGTCTCCAT	GCTGGTCCCC
						c
	430	440	450	460	470	480
Marra EST	ccaCCCAaAGG	-aCCCATCAT	CACCAaCaAC	CGtTTCACCT	aTgccAGtTA	-cAaCAGcat>
SEQ03_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC
	250	260	270	280	290	300
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GGGAACCTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTGATTC	GGGGAACATC
	CCCTTGAAGT	GGAGCCTCTA	CTAGTAGGTG	TTACACCTCG	GGTCACTAAG	CCCCTTGTAG
	490	500	510	520		
Marra EST	GacAgCTTCA	tCTCGGAGtT	GATCATCCAt	gATGTGcAGC	CCAGTG>	
SEQ03_ORF	GGGAACCTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTG	

	310	320	330	340	350	360
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	AGATGCAGCC	TCCAGAACAG	TCGCCTGCAT	GGATCTGCTT	ACCTTACCGT	CCAAGTTATG
	TCTACGTCGG	AGGTCTTGTC	AGCGGACGTA	CCTAGACGAA	TGGAATGGCA	GGTTCAATAC
	370	380	390	400	410	420
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GGAGAGCTGT	TCATTCCCAG	TGTTAATCTT	GTAGTCGCTG	AGAATGAACC	TTGTGAAGTT
	CCTCTCGACA	AGTAAGGGTC	ACAATTAGAA	CATCAGCGAC	TCTTACTTGG	AACACTTCAA
	430	440	450	460	470	480
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	ACTTGCTCTAC	CCTCACACTG	GACCTGGCTC	CCGGATATTT	CCTGGGAGCT	CGGTCTCCTG
	TGAACAGATG	GGAGTGTGAC	CTGGACCGAG	GGCCTATAAA	GGACCCTCGA	GCCAGAGGAC
	490	500	510	520	530	540
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GTCAGCCATT	CAAGCTATTA	TTTGTTCCTG	GAGCCCAGCG	ACCTTCAAAG	TGCAGTGAGC
	CAGTCGGTAA	GTTCGATAAT	AAAACAAGGC	CTCGGGTCGC	TGGAAGTTTC	ACGTCACTCG
	550	560	570	580	590	600
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	ATCCTGGCTC	TGACCCACAC	GAGCAATGGG	ACTTTGACTT	GCGTGGCTAC	CTGGAAGAGC
	TAGGACCGAG	ACTGGGGTGT	CTCGTTACCC	TGAAACTGAA	CGCACCAGATG	GACCTTCTCG
	610	620	630	640	650	660
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	CTGAAGGCC	GCAAGTCTGC	AACTGTAAAT	CTCACTGTGA	TTCGGTGTCC	CCAAGACACT
	GACTTCCGGG	CGTTCAGACG	TTGACATTTA	GAGTGACACT	AAGCCACAGG	GGTTCTGTGA
	670	680	690	700	710	720
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GGAGGTGGTA	TTAATATTCC	AGGTGTATTA	TCAAGTTTAC	CGAGTTTAGG	TTTTTCATTG
	CCTCCACCAT	AATTATAAGG	TCCACATAAT	AGTTCAAATG	GCTCAAATCC	AAAAAGTAAC
	730	740	750	760	770	780
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	CCTACTTGGG	GCAAAGTTGG	ACTTGGAATA	GCAGGCACCA	TGCTTCTGAC	GCCGACGTGT
	GGATGAACCC	CGTTTCAACC	TGAACCTGAT	CGTCCGTGGT	ACGAAGACTG	CGGCTGCACA
	790	800	810	820	830	840
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	ACTCTTACAA	TACGCTGCTG	CTGCTGCCGC	CGTCGTTGTT	GTGGCTGCAA	CTGCTGCTGC
	TGAGAATGTT	ATGCGACGAC	GACGACGGCG	GCAGCAACAA	CACCGACGTT	GACGACGACG
	850	860	870	880	890	900
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	CGTTGTTGTT	TCTGCTGTAG	AAGAAAAAGA	GGATTTTCGT	TTCAATTTCA	AAAGAAATCT
	GCAACAACAA	AGACGACATC	TTCTTTTCT	CCTAAAGCAT	AAGTTAAAGT	TTTCTTTAGA

	910	920	930	940	950	960
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	GAAAAAGAGA	AGACAAACAA	AGAAACTGAG	ACAGAAAGTG	GAAATGAAAA	CTCCGGCTAC
	CTTTTCTCT	TCTGTTTGTT	TCTTTGACTC	TGTCTTTCAC	CTTTACTTTT	GAGGCCGATG
	970	980	990	1000	1010	1020
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	AATTCAGATG	AACAAAAGAC	CACAGACACC	GCTTCTCTCC	CTCCCAAATC	CTGTGAATCC
	TTAAGTCTAC	TTGTTTTCTG	GTGTCTGTGG	CGAAGAGAGG	GAGGGTTTAG	GACACTTAGG
	1030	1040	1050	1060	1070	1080
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	AGTGATCCTG	AACAAAGAAA	CAGTAGCTGT	GGCCCTCCTC	ACCAGCGGGC	TGATCAACGT
	TCACTAGGAC	TTGTTTCTTT	GTCATCGACA	CCGGGAGGAG	TGGTCGCCCC	ACTAGTTGCA
	1090	1100	1110	1120	1130	1140
	* *	* *	* *	* *	* *	* *
SEQ03_ORF	CCACCCAGGC	CAGCAAGTCA	TCCACAGGCT	TCTTTTAATC	TGGCCAGTCC	TGAGAAGGTC
	GGTGGGTCCG	GTCGTTCAGT	AGGTGTCCGA	AGAAAATTAG	ACCGGTCAGG	ACTCTTCCAG
	1150					
	* *	*				
SEQ03_ORF	AGTAATACAA	CTGTAGTA				
	TCATTATGTT	GACATCAT				

EXHIBIT C

	10	20	30	40	50	60
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	ATGGAAGGC	ATTTGCTCAC	GGTCCAGAA	GCTGTAGGT	CTGGGTCTGG	TAATGAAGTC
	TACCTTTCCG	TAAACGAGTG	CCAAGGTCTT	CGACATCCAA	GACCCAGACC	ATTACTTCAG
	250	260	270	280	290	300
Marra EST	cTGGctgtGC	tggTcaTCct	GGc-tCAGct	--gacAGcTT	CcGGaTCcaG	TtATcAgaTC>
SEQ05_ORF	ATGGAAGGC	ATTTGCTCAC	GGTCCAGAA	GCTGTAGGT	CTGGGTCTGG	TAATGAAGTC
	70	80	90	100	110	120
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	ATAGAAGGCC	CCCAGAATGC	AACAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC
	TATCTTCCGG	GGGTCTTACG	TTGTCAGGAC	TTCCCAGAGG	TCCGAGCGAA	GTTGACGTGG
	310	320	330	340	350	360
Marra EST	ATAGAAGGtC	CtCAGAATGt	AACAGTCCTa	AAGGaCTCag	AGGCTCaCTT	CAACTGCACC>
SEQ05_ORF	ATAGAAGGCC	CCCAGAATGC	AACAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC
	130	140	150	160	170	180
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC
	CAGAGGGTCC	CGACCTTCGA	GTAGTACACC	CGAGAGTCAC	TGTACCACCA	CGATTTCGAG
						a
	370	380	390	400	410	420
Marra EST	GTGaCtCaCg	GCTGGAAGCT	tcTCATGTGG	aCTCTtAacc	AaATGGTGGT	GCTgAGtcTC>
SEQ05_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC
	190	200	210	220	230	240
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC
	TCCGGGTACC	TCGGGTAGTA	GTGGTTACTG	GCGAAGTGGA	GAGTCTCCAT	GCTGGTCCCCG
						c
	430	440	450	460	470	480
Marra EST	ccaCCCAaGg	-aCCCATCAT	CACCAaCaAC	CGtTTCACCT	aTgccAGtTA	-cAaCAGcat>
SEQ05_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC
	250	260	270	280	290	300
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	GGGAACCTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTGATTC	GGGGAACATC
	CCCTTGAAGT	GGAGCCTCTA	CTAGTAGGTG	TTACACCTCG	GGTCACTAAG	CCCCTTGTAG
	490	500	510	520		
Marra EST	GacAgCTTCA	tCTCGGAGtT	GATCATCCAt	gATGTGcAGC	CCAGTG>	
SEQ05_ORF	GGGAACCTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTG	

	310	320	330	340	350	360
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	AGATGCAGCC	TCCAGAACAG	TCGCCTGCAT	GGATCTGCTT	ACCTTACCGT	CCAAGTTATG
	TCTACGTCGG	AGGTCTTGTC	AGCGGACGTA	CCTAGACGAA	TGGAATGGCA	GGTTCAATAC
	370	380	390	400	410	420
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	GGAGAGCTGT	TCATTCCCAG	TGTTAATCTT	GTAGTCGCTG	AGAATGAACC	TTGTGAAGTT
	CCTCTCGACA	AGTAAGGGTC	ACAATTAGAA	CATCAGCGAC	TCTTACTTGG	AACACTTCAA
	430	440	450	460	470	480
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	ACTTGTCTAC	CCTCACACTG	GACCCGGCTC	CCGGATATTT	CCTGGGAGCT	CGGTCTCCTG
	TGAACAGATG	GGAGTGTGAC	CTGGGCCGAG	GGCCTATAAA	GGACCCTCGA	GCCAGAGGAC
	490	500	510	520	530	540
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	GTCAGCCATT	CAAGCTATTA	TTTTGTTCCT	GAGCCCAGCG	ACCTTCAAAG	TGCAGTGAGC
	CAGTCGGTAA	GTTTCGATAA	AAAACAAGGC	CTCGGGTCGC	TGGAAGTTTC	ACGTCACTCG
	550	560	570	580	590	600
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	ATCCTGGCTC	TGACCCACAC	GAGCAATGGG	ACTTTGACTT	GCGTGGCTAC	CTGGAAGAGC
	TAGGACCGAG	ACTGGGGTGT	CTCGTTACCC	TGAAACTGAA	CGCACCAGATG	GACCTTCTCG
	610	620	630	640	650	660
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	CTGAAGGCCC	GCAAGTCTGC	AACTGTAAAT	CTCACTGTGA	TTCGGTGTCC	CCAAGACACT
	GACTTCCGGG	CGTTCAGACG	TTGACATTTA	GAGTGACACT	AAGCCACAGG	GGTTCTGTGA
	670	680	690	700	710	720
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	GGAGGTGGTA	TTAATATTCC	AGGTGTATTA	TCAAGTTTAC	CGAGTTTAGG	TTTTTCATTG
	CCTCCACCAT	AATTATAAGG	TCCACATAAT	AGTTCAAATG	GCTCAAATCC	AAAAAGTAAC
	730	740	750	760	770	780
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	CCTACTTGGG	GCAAAGTTGG	ACTTGGACTA	GCAGGCACCA	TGCTTCTGAC	GCCGACGTGT
	GGATGAACCC	CGTTTCAACC	TGAACCTGAT	CGTCCGTGGT	ACGAAGACTG	CGGCTGCACA
	790	800	810	820	830	840
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	ACTCTTACAA	TACGCTGCTG	CTGCTGCCGC	CGTCGTTGTT	GTGGCTGCAA	CTGCTGCTGC
	TGAGAATGTT	ATGCGACGAC	GACGACGGCG	GCAGCAACAA	CACCGACGTT	GACGACGACG
	850	860	870	880	890	900
	* * * *	* *	* *	* *	* *	* *
SEQ05_ORF	CGTTGTTGTT	TCTGCTGTAG	AAGAAAAAGA	GGATTTCGTA	TTCAATTTCA	AAAGAAATCT
	GCAACAACAA	AGACGACATC	TTCTTTTTCT	CCTAAAGCAT	AAGTTAAAGT	TTTCTTTAGA

	910	920	930	940	950	960
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	GAAAAAGAGA	AGACAAACAA	AGAAACTGAG	ACAGAAAGTG	GAAATGAAAA	CTCCGGCTAC
	CTTTTCTCT	TCTGTTTGTT	TCTTTGACTC	TGTCTTTCAC	CTTTACTTTT	GAGGCCGATG
	970	980	990	1000	1010	1020
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	AATTCAGATG	AACAAAAGAC	CACAGAAACC	GCTTCTCTCC	CTCCCAAATC	CTGTGAATCC
	TTAAGTCTAC	TTGTTTTCTG	GTGTCTTTGG	CGAAGAGAGG	GAGGGTTTAG	GACACTTAGG
	1030	1040	1050	1060	1070	1080
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	AGTGATCCTG	AACAAAGAAA	CAGTAGCTGT	GGCCCTCCTC	ACCAGCGGGC	TGATCAACGT
	TCACTAGGAC	TTGTTTCTTT	GTCATCGACA	CCGGGAGGAG	TGGTCGCCCC	ACTAGTTGCA
	1090	1100	1110	1120	1130	1140
	* *	* *	* *	* *	* *	* *
SEQ05_ORF	CCACCCAGGC	CAGCAAGTCA	TCCACAGGCT	TCTTTTAATC	TGGCCAGTCC	TGAGAAGGTC
	GGTGGGTCCG	GTCGTTCACT	AGGTGTCCGA	AGAAAATTAG	ACCGGTCAGG	ACTCTTCCAG
	1150					
	* *					
SEQ05_ORF	AGTAATACAA	CTGTAGTA				
	TCATTATGTT	GACATCAT				

EXHIBIT D

	44210	44220	44230	44240	44250
AF121782	AGAAAGGTTACAGCACACAGTTGATTTATGGAGATCCATTCATTTAACAA				
	TCTTTCCAATGTCGTGTGTCAACTAAATACCTCTAGGTAAGTAAATTGTT				

44260 44270 44280 44290 44300
AF121782 CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATA
 GAACTTTTTTAACCGATGGAAGGTCCAAGACCCAGACCATTACTTCAGTAT

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1. SEQ01_ORF 10          20          30          40          50
[ 1598 ]      CTTG--TGATT---TTCCTCCACGGTCTCTGGGTCTGGTAATGAAGTCATA>
              ||||      |||      |||      |||      |||||
AF121782      CTTGAAAAATTGGCTACCTCCAGGTCTCTGGGTCTGGTAATGAAGTCATA

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	44310	44320	44330	44340	44350
AF121782	GAAGGCCCCCAAAATGCAAGAGTCTCTGAAGGGCTCCCAGGCTCGCTTCAA				
	CTTCCGGGGGGTTTTACGTTCTCAGGACTTCCCCAGGGTCCGAGCGAAGTT				

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1. SEQ01_ORF      60      70      80      90     100
[ 1598 ]      GAAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA>
                |||||
AF121782      GAAGGCCCCCAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA

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44360 44370 44380 44390 44400
AF121782 CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA
GACGTGGCAGAGGGTCCCACCTTCGAGTAGTACACCCGAGAGTCACTGT

```

1. SEQ01_ORF      110      120      130      140      150
[ 1598 ] CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA>
          |||||
AF121782 CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA

```

44410 44420 44430 44440 44450
 AF121782 TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGC
 ACCACCACGATTTCGCAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCG

```

1. SEQ01_ORF      160      170      180      190      200
[ 1598 ]  TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGC>
          |||||
AF121782  TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGC

```

44460 44470 44480 44490 44500
AF121782 TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT
 AAGTGGAGAGTCTCCATGCTGGTCCCGCCCTTGAAGTGGAGCCTCTACTA

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1. SEQ01_ORF      210      220      230      240      250
[ 1598 ]          TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT>
                  |||
AF121782          TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT

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          44510      44520      44530      44540      44550
AF121782  CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC
          GTAGGTGTTACACCTCGGGTCACCTAAGCCCCCTGTAGTCTACGTCGGAGG

1. SEQ01_ORF      260      270      280      290      300
[ 1598 ] CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC>
          |||||
AF121782  CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC

          44560      44570      44580      44590      44600
AF121782  AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTGTAT
          TCTTGTTCAGCGGACGTACCTAGACGAATGGAATGGCAGGTTCCACACATA

1. SEQ01_ORF      310      320      330      340
[ 1598 ] AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAA-GT-T--AT>
          |||||
AF121782  AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTGTAT

          44610      44620      44630      44640      44650
AF121782  GCAGGTGGCTTCTGAAGTCCATCAGGTTAAATGTCAGAGGGCAGGAAGGA
          CGTCCACCGAAGACTTCAGGTAGTCCAATTTACAGTCTCCCGTCCTTCCT

          T      TC
          |      |
1. SEQ01_ORF      350      360      370      |      380      390
[ 1598 ] G--GGAGAGCTGTTTCATTCC--CAGGTTAATTGTAGTCGCTGAGAATGAA>
          | ||| | ||| | ||| ||||| ||| | ||| | |||
AF121782  GCAGGTGGCTTCTGAAGTCCATCAGGTTAAATGTCAGAGGGCAGGAAGGA

          44660      44670      44680      44690      44700
AF121782  CCTTCTAAAGTTCATGCCGCGTATGATGGCAGACGTGGTCTACCTTCAGT
          GGAAGATTTCAAGTACGGCGCATACTACCGTCTGCACCAGATGGAAGTCA

          A      G
          |      |
1. SEQ01_ORF      400      410      420      430      440
[ 1598 ] CCTTGTGAAGTTCCTTGTCTACCTCACACTGGACCCGG-CTCCCGATATT>
          |||| | ||||| ||| | ||| ||||| ||| |||
AF121782  CCTTCTAAAGTTCATGCCGCGTATGATGGCAGACGTGGTCTACCTTCAGT

          44710      44720      44730      44740      44750
AF121782  TGGTGTTGACCTACAATTATTCTGAACTGATGAATGTTTTGCGATTTATT
          ACCACAACCTGGATGTTAATAAGACTTGACTACTTACAAAACGCTAAATAA

          CC
          |
1. SEQ01_ORF      450      460      470      |      480      490
[ 1598 ] TCCTG-GGAGCT-C-GGTCTCCTGGTCAGATTCAAGCTAT--TATTTTGT>
          | || |||| | |||| | ||| ||||| |||||
AF121782  TGGTGTTGACCTACAATTATTCTGAACTGATGAATGTTTTGCGATTTATT

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44760 44770 44780 44790 44800
 AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC
 ACAGCGGAGGAAGGAGGGAGTACGAGAGGGATGGAGGAGTGAAGAAGAAG

A
 |
 1. SEQ01_ORF 500 510 520 530 540
 [1598] TCCGGAGCCCAGCGACCTTCAAGTGCAGTGAGCATCCTGGCTCTGACCCC>
 | | | | | | | | | | | | | | | | | |
 AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC

44810 44820 44830 44840 44850
 AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT
 GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAACCGTTA

1. SEQ01_ORF 550 560 570 580 590
 [1598] ACAGAGCAATGGGACTT-TGACTTGCGTG-GCTA-CCTGGAAGAGCCTGA>
 | | | | | | | | | | | | | | | | | |
 AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT

44860 44870 44880 44890 44900
 AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA
 TCCGAATCTTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT

G TCCCCA
 | |
 1. SEQ01_ORF 600 610 620 630
 [1598] AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTTCGGTGAGACA>
 | | | | | | | | | | | | | | | | | |
 AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA

44910 44920 44930 44940 44950
 AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCTGCTTCATT
 AGGGGGAAGAAGGAGTGAAGGAGGGTAGAAAGGGAAAAAGGACGAAGTAA

T
 |
 1. SEQ01_ORF 650 660 670 680 690
 [1598] CTGGAGGTGGTATTAAATTCAGGTGTATTATCAAGTTTACCGAGT--TT>
 | | | | | | | | | | | | | | | | | |
 AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCTGCTTCATT

44960 44970 44980 44990 45000
 AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTCTGGTTAAGACTGATAG
 GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAAGACCAATTCTGACTATC

1. SEQ01_ORF 700 710 720 730 740
 [1598] AGGTTTTTCATTGCCTACTTG--GGGCAAAGTTGGACTT-GGACTAGCAG>
 | | | | | | | | | | | | | | | | | |
 AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTCTGGTTAAGACTGATAG

45260 45270 45280 45290 45300
 AF121782 ACCCTGCCTCCAACCTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT
 TGGGACGGAGGTTGATGTCACCTATCAGTAATATCAGTTTCAACACACA

A AGC GGCC
 | |
 1. SEQ01_ORF | 1000 1010 1020 1030 | |
 [1598] CCCAATCCTGTGAATCCAGT--GATCCTGAACAAAGAAACAGTTGTCTCC>
 || ||| | | ||| ||| | | ||| | ||||| |
 AF121782 ACCCTGCCTCCAACCTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT

45310 45320 45330 45340 45350
 AF121782 TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT
 AGTGGTTTATATAGTTCAGTAACTCTCTTTTCTTTTCTTATTTGTTTTAA

GCG C
 | |
 1. SEQ01_ORF1050 | 1060 | 1070 1080 1090
 [1598] TCACCAGGCTGATCAAGTC-CACCCAGGCCAGCAAGTCATCCAC-AGGCT>
 ||||| ||||| || ||| || ||| |
 AF121782 TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT

45360 45370 45380 45390 45400
 AF121782 TATAATAATAGCTTATTTTTTCATTTTAGAGGTAATTTGGAGGTGCTGAAG
 ATATTATTATCGAATAAAAAGTAAAATCTCCATTAAACCTCCACGACTTC

1. SEQ01_ORF1100 1110 1120 1130 1140
 [1598] TCTTTTAAT--CTGGCCAGTCCTGAGA-AGGTCAGTAATA-CAACTGTAG>
 | | |||| | || | | |||| | | | ||| |
 AF121782 TATAATAATAGCTTATTTTTTCATTTTAGAGGTAATTTGGAGGTGCTGAAG

45410 45420 45430 45440 45450
 AF121782 ATAATGTTACACAGTAAAAAAGTAAAAGGATGCTTTACAAAGATTTGGAA
 TATTACAATGTGTCATTTTTTTCATTTTCCTACGAAATGTTTCTAAACCTT

1. SEQ01_ORF
 [1598] -TA>
 ||
 AF121782 ATA

45460 45470 45480 45490 45500
 AF121782 TAGTCTTACCAAATTTAATCACTTTGCATTCTTTAAAAGTGATTTTATA
 ATCAGAATGGTTTTAAATTAGTGAAACGTAAGAAATTTTCACATAAATAT

EXHIBIT E

	44210	44220	44230	44240	44250
AF121782	AGAAAGGTTACAGCACACAGTTGATTTATGGAGATCCATTCATTTAACAA				
	TCTTTCCAATGTCGTGTGTCAACTAAATACCTCTAGGTAAGTAAATTGTT				

AF121782 44260 44270 44280 44290 44300
CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATA
GAACTTTTTTAACCGATGGAAGGTCCAAGACCCAGACCATTACTTCAGTAT

```

1. SEQ03_ORF      20          30          40          50          60
[ 1636 ] CATGGAAAA-TAGAGACCCACCCGGTCTGGGTCTGGTAATGAAGTCATA>
               | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AF121782 CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATA

```

	44310	44320	44330	44340	44350
AF121782	GAAGGCCCCCAAATGCAAGAGTCTCTGAAGGGCTCCAGGCTCGCTTCAA				
	CTTCCGGGGGTTTTACGTTCTCAGGACTTCCCGAGGGTCCGAGCGAAGTT				

```

1. SEQ03_ORF      70      80      90     100     110
[ 1636 ]      GAAGGCCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA>
                |||||
AF121782      GAAGGCCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA

```

	44360	44370	44380	44390	44400
AF121782	CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA				
	GACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGT				

```

1. SEQ03_ORF      120      130      140      150      160
[ 1636 ]      CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA>
                |||||
AF121782      CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA

```

AF121782 44410 44420 44430 44440 44450
TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGC
ACCACCACGATTTCGCAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCG

```

1. SEQ03_ORF      170      180      190      200      210
[ 1636 ]      TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATGACCGC>
                |||||
AF121782      TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATGACCGC

```

44460 44470 44480 44490 44500
AF121782 TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTCACCTCGGAGATGAT
AAGTGGAGAGTCTCCATGCTGGTCCCGCCCTTGAAGTGGAGCCTCTACTA

```

1. SEQ03_ORF      220      230      240      250      260
[ 1636 ]      TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT>
                |||||
AF121782      TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT

```


44760 44770 44780 44790 44800
 AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC
 ACAGCGGAGGAAGGAGGGAGTACGAGAGGGATGGAGGAGTGAAGAAGAAG

A
 |
 1. SEQ03_ORF 510 520 530 540 550
 [1636] TCCGGAGCCCAGCGACCTTCAAGTGCAGTGAGCATCCTGGCTCTGACCCC>
 | | | | | | | | | | | | | | | | | | | | | |
 AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC

44810 44820 44830 44840 44850
 AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT
 GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAACCGTTA

1. SEQ03_ORF560 570 580 590 600
 [1636] ACAGAGCAATGGGACTT-TGACTTGCGTG-GCTA-CCTGGAAGAGCCTGA>
 | | | | | | | | | | | | | | | | | | | | | |
 AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT

44860 44870 44880 44890 44900
 AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA
 TCCGAATCTTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT

G TCCCCA
 | |
 1. SEQ03_ORF 610 620 630 640
 [1636] AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTCCGGTGAGACA>
 | | | | | | | | | | | | | | | | | | | | | |
 AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA

44910 44920 44930 44940 44950
 AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCTGCTTCATT
 AGGGGGAAGAAGGAGTGAAGGAGGGTAGAAAGGGAAAAAGACGAAGTAA

T
 |
 1. SEQ03_ORF660 670 680 690 700
 [1636] CTGGAGGTGGTATTAAATTCCAGGTGTATTATCAAGTTTACCGAGT--TT>
 | | | | | | | | | | | | | | | | | | | | | |
 AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCTGCTTCATT

44960 44970 44980 44990 45000
 AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTTCTGGTTAAGACTGATAG
 GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAAGACCAATTCTGACTATC

1. SEQ03_ORF710 720 730 740 750
 [1636] AGGTTTTTCATTGCCTACTTG--GGGCAAAGTTGGACTT-GGACTAGCAG>
 | | | | | | | | | | | | | | | | | | | | | |
 AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTTCTGGTTAAGACTGATAG

	45010	45020	45030	45040	45050
AF121782	AGACAGATTTTATCACTTCCCCTTTGAATCCATTTTAGTATTTAACAGCC				
	TCTGTCTAAAATAGTGAAGGGGAACTTAGGTAAAATCATAAATTGTCGG				
1. SEQ03_ORF	760	770	780	790	800
[1636]	GCACCATGCTTCTGAC-GCCGACGTGTA-CTCTTACAATACGCTGCTG-C>				
AF121782	AGACAGATTTTATCACTTCCCCTTTGAATCCATTTTAGTATTTAACAGCC				
	45060	45070	45080	45090	45100
AF121782	TTTCTGGAAACGTATCCTGGAATTCTTCTAGGGCCAGTTGCAGTCATTTT				
	AAAGACCTTTGCATAGGACCTTAAGAAGATCCCGGTCAACGTCAGTAAAA				
		C			
1. SEQ03_ORF	810	820	830	840	
[1636]	T-GCTGCCGCCGTGTTGTTG-TGGCTGCAACTG-CTGCTGCCGTTGTTGT>				
AF121782	TTTCTGGAAACGTATCCTGGAATTCTTCTAGGGCCAGTTGCAGTCATTTT				
	45110	45120	45130	45140	45150
AF121782	TCTTTGATTTAGAGACAGTTGTCAATCACTGCCCTTTCTCTAGTTTTTCC				
	AGAAACTAAATCTCTGTCAACAGTTAGTGACGGGAAAGAGATCAAAAAGG				
		AAG		AA	
1. SEQ03_ORF	860	870	880	890	900
[1636]	T-TCTGCTGTAGAAAAAGAGGATTTTCGTATTCAATTTCAAAGATCTGAA>				
AF121782	TCTTTGATTTAGAGACAGTTGTCAATCACTGCCCTTTCTCTAGTTTTTCC				
	45160	45170	45180	45190	45200
AF121782	ATATACATGACTATATTTCTCTGCTTGCAATCATTTATCAACTCTGAAGCA				
	TATATGTACTGATATAAAGAGACGAACGTAGTAAATAGTTGAGACTTCGT				
1. SEQ03_ORF	910	920	930	940	950
[1636]	AAAGAGAAGAC-AAACAAAGAAAC-TGAGACAGAAAGTGGAATGAAAAC>				
AF121782	ATATACATGACTATATTTCTCTGCTTGCAATCATTTATCAACTCTGAAGCA				
	45210	45220	45230	45240	45250
AF121782	TGCTTTAACTCTTTCCTCTTCCAGCAGAATCCCCCAACTTATTTCTCT				
	ACGAAATTGAGAAAGGAGAAAGGTCGTCTTAGGGGGTTGAATAAAGAGA				
			CC		
1. SEQ03_ORF	960	970	990	1000	
[1636]	TCCGGCTAC-AATTCAGATGAACAAAAGAACAGACACCGCTTCTCTCCCT>				
AF121782	TGCTTTAACTCTTTCCTCTTCCAGCAGAATCCCCCAACTTATTTCTCT				

45260 45270 45280 45290 45300
 AF121782 ACCCTGCCTCCAACTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT
 TGGGACGGAGGTTGATGTCACCCTATCAGTAATATCAGTTTCAACACACA

A AGC GGCC
 | |
 1. SEQ03_ORF |1010 1020 1030 1040 1050
 [1636] CCCAATCCTGTGAATCCAGT--GATCCTGAACAAAGAAACAGTTGTCTCC>
 || ||| | | |||| ||| | | | ||| ||||| |
 AF121782 ACCCTGCCTCCAACTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT

45310 45320 45330 45340 45350
 AF121782 TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT
 AGTGGTTTATATAGTTCAGTAACTCTCTTTTCTTTTCTTATTTGTTTTAA

GCG C
 | |
 1. SEQ03_ORF 1060 1070 1080 1090 1100 1110
 [1636] TCACCAGGCTGATCAAGTC-CACCCAGGCCAGCAAGTCATCCAC-AGGCT>
 ||||| ||||| || ||| || ||| | |
 AF121782 TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT

45360 45370 45380 45390 45400
 AF121782 TATAATAATAGCTTATTTTTTCATTTTAGAGGTAATTTGGAGGTGCTGAAG
 ATATTATTATCGAATAAAAAGTAAATCTCCATTAAACCTCCACGACTTC

1. SEQ03_ORF 1120 1130 1140 1150
 [1636] TCTTTTAAT--CTGGCCAGTCCTGAGA-AGGTCAGTAATA-CAACTGTAG>
 | | |||| | || | | |||| | | | ||| ||
 AF121782 TATAATAATAGCTTATTTTTTCATTTTAGAGGTAATTTGGAGGTGCTGAAG

45410 45420 45430 45440 45450
 AF121782 ATAATGTTACACAGTAAAAAAGTAAAAGGATGCTTTACAAAGATTTGGAA
 TATTACAATGTGTCAATTTTTTCATTTTCCTACGAAATGTTTCTAAACCTT

1. SEQ03_ORF
 [1636] -TA>
 ||
 AF121782 ATA

45460 45470 45480 45490 45500
 AF121782 TAGTCTTACCAAATTTAATCACTTTGCATTCTTTAAAAGTGATTTTATA
 ATCAGAATGGTTTTAAATTAGTGAAACGTAAGAAATTTTCACATAAATAT

EXHIBIT F

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      44160      44170      44180      44190      44200
AF121782  ACAGTCTGAGTCACTGGATGGACAACCTGGGGGTACCAGTGGTAAATAC
          TGTCAGACTCAGTGACCTACCTGTTGGACCCCCAATGGTGACCATTATG

      44210      44220      44230      44240      44250
AF121782  AGAAAGGTTACAGCACACAGTTGATTTATGGAGATCCATTCAATTAACAA
          TCTTTCCAATGTCGTGTGTCAACTAAATACCTCTAGGTAAGTAAATTGTT

1. SEQ05_ORF      10      20
[ 1596 ]          ATGGAAAGGCATT-TGCTCAC-G>
                  ||||| | ||| | ||
AF121782          ATGGAGATCCATTCAATTAACAA

      44260      44270      44280      44290      44300
AF121782  CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATA
          GAACTTTTAAACCGATGGAAGGTCCAAGACCCAGACCATTACTTCAGTAT

1. SEQ05_ORF      30      40      50      60
[ 1596 ]          GTTCCAGAA---GC-----TGTAGGTTCTGGGTCTGGTAATGAAGTCATA>
                  || | || || | ||||| ||||| ||||| ||||| |||||
AF121782          CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGTCTGGTAATGAAGTCATA

      44310      44320      44330      44340      44350
AF121782  GAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA
          CTTCCGGGGGTTTTACGTTCTCAGGACTTCCCGAGGGTCCGAGCGAAGTT

1. SEQ05_ORF      70      80      90      100      110
[ 1596 ]          GAAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA>
                  ||||| ||||| ||||| ||||| ||||| ||||| |||||
AF121782          GAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAA

      44360      44370      44380      44390      44400
AF121782  CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA
          GACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGT

1. SEQ05_ORF      120      130      140      150      160
[ 1596 ]          CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA>
                  ||||| ||||| ||||| ||||| ||||| ||||| |||||
AF121782          CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACA

      44410      44420      44430      44440      44450
AF121782  TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATGACCGC
          ACCACCACGATTTCGCAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCG

1. SEQ05_ORF      170      180      190      200      210
[ 1596 ]          TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATGACCGC>
                  ||||| ||||| ||||| ||||| ||||| ||||| |||||
AF121782          TGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACC AATGACCGC
```

44460 44470 44480 44490 44500
 AF121782 TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT
 AAGTGGAGAGTCTCCATGCTGGTCCC GCCCTTGAAGTGGAGCCTCTACTA

1. SEQ05_ORF 220 230 240 250 260
 [1596] TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT>
 |||||
 AF121782 TTCACCTCTCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGAT

44510 44520 44530 44540 44550
 AF121782 CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC
 GTAGGTGTTACACCTCGGGTCACTAAGCCCCTTGTAGTCTACGTCGGAGG

1. SEQ05_ORF 270 280 290 300 310
 [1596] CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC>
 |||||
 AF121782 CATCCACAATGTGGAGCCCAGTGATTTCGGGGAACATCAGATGCAGCCTCC

44560 44570 44580 44590 44600
 AF121782 AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTGTAT
 TCTTGTGACGGACGTACCTAGACGAATGGAATGGCAGGTTCCACACATA

1. SEQ05_ORF 320 330 340 350
 [1596] AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAA-GT-T--AT>
 ||||| || ||
 AF121782 AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTGTAT

44610 44620 44630 44640 44650
 AF121782 GCAGGTGGCTTCTGAAGTCCATCAGGTTAAATGTCAGAGGGCAGGAAGGA
 CGTCCACCGAAGACTTCAGGTAGTCCAATTTACAGTCTCCCGTCCTTCCT

T TC
 | |
 1. SEQ05_ORF 370 380 390 400
 [1596] G--GGAGAGCTGTTTCATTCC--CAGGTTAATTGTAGTCGCTGAGAATGAA>
 | || | ||| ||||| ||| | |||
 AF121782 GCAGGTGGCTTCTGAAGTCCATCAGGTTAAATGTCAGAGGGCAGGAAGGA

44660 44670 44680 44690 44700
 AF121782 CCTTCTAAAGTTCATGCCGCGTATGATGGCAGACGTGGTCTACCTTCAGT
 GGAAGATTTCAAGTACGGCGCATACTACCGTCTGCACCAGATGGAAGTCA

A G
 | |
 1. SEQ05_ORF 420 430 440 450
 [1596] CCTTGTGAAGTTCCTTGTCTACCTCACA CTGGACCCGG-CTCCCGATATT>
 |||| | ||||| || | || |||||
 AF121782 CCTTCTAAAGTTCATGCCGCGTATGATGGCAGACGTGGTCTACCTTCAGT

44710 44720 44730 44740 44750
AF121782 TGGTGTGACCTACAATTATTCTGAACTGATGAATGTTTTGCGATTTATT
ACCACAACCTGGATGTTAATAAGACTTGACTACTTACAAAACGCTAAATAA

CC
|
1. SEQ05_O460 470 480 490 500
[1596] TCCTG-GGAGCT-C-GGTCTCCTGGTCAGATTCAAGCTAT--TATTTTGT>
| | | | | | | | | | | | | | | |
AF121782 TGGTGTGACCTACAATTATTCTGAACTGATGAATGTTTTGCGATTTATT

44760 44770 44780 44790 44800
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC
ACAGCGGAGGAAGGAGGGAGTACGAGAGGGATGGAGGAGTGAAGAAGAAG

A
|
1. SEQ05_ORF 510 520 530 540 550
[1596] TCCGGAGCCCAGCGACCTTCAAGTGCAGTGAGCATCCTGGCTCTGACCCC>
| | | | | | | | | | | | | | | |
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC

44810 44820 44830 44840 44850
AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT
GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAACCGTTA

1. SEQ05_ORF560 570 580 590 600
[1596] ACAGAGCAATGGGACTT-TGACTTGCGTG-GCTA-CCTGGAAGAGCCTGA>
| | | | | | | | | | | | | | | |
AF121782 CCTTCTCCCCCTCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT

44860 44870 44880 44890 44900
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA
TCCGAATCTTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT

G TCCCCA
| |
1. SEQ05_ORF 610 620 630 640
[1596] AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTCCGGTGAGACA>
| | | | | | | | | | | | | | | |
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTTATTGTTTCGTTGATTTA

44910 44920 44930 44940 44950
AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCCTGCTTCATT
AGGGGGAAGAAGGAGTGAAGGAGGGTAGAAAGGGAAAAAGGACGAAGTAA

T
|
1. SEQ05_OR660 670 680 690 700
[1596] CTGGAGGTGGTATTAAATTCCAGGTGTATTATCAAGTTTACCGAGT--TT>
| | | | | | | | | | | | | | | |
AF121782 TCCCCCTTCTTCCTCACTTCCTCCCATCTTTCCCTTTTTCCTGCTTCATT

AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTTCTGGTTAAGACTGATAG
GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAGACCAATTCTGACTATC

1. SEQ05_ORF [1596]
720 730 740 750
AGGTTTTTCATTGCCTACTTG--GGGCAAAGTTGGACTT-GGACTAGCAG>
||| || || | | ||| | || || ||| ||

AF121782 CTCTTTCTCCTTCCATCTTTGCTTTTCCTTTTTTCTGGTTAAGACTGATAG

AF121782 45010 45020 45030 45040 45050
AGACAGATTTTATCACTTCCCCTTTGAATCCATTTTAGTATTTAACAGCC
TCTGTCTAAAATAGTGAAGGGGAAACTTAGGTAAAATCATAAATTGTCGG

1. SEQ05_ORF [1596]
760 770 780 790 800
GCACCATGCTTCTGAC-GCCGACGTGTA-CTCTTACAATACGCTGCTG-C>
|| || | || || || | | || | || | | |

AF121782 AGACAGATTTTATCACTTCCCCTTTGAATCCATTTTAGTATTTAACAGCC

AF121782 45060 45070 45080 45090 45100
TTTCTGGAAACGTATCCTGGAATTCTTCTAGGGCCAGTTGCAGTCATTTT
AAAGACCTTTGCATAGGACCTTAAGAAGATCCCGGTCAACGTCAGTAAAA

1. SEQ05_ORF [1596]
810 C | 820 830 840
T-GCTGCCGCCGTGTTGTTG-TGGCTGCAACTG-CTGCTGCCGTTGTTGT>
| ||| ||| | | | || | | | | | | | | |

AF121782 TTTCTGGAAACGTATCCTGGAATTCTTCTAGGGCCAGTTGCAGTCATTTT

AF121782 45110 45120 45130 45140 45150
TCTTTGATTTAGAGACAGTTGTCAATCACTGCCCTTTCTCTAGTTTTTCC
AGAAACTAAATCTCTGTCAACAGTTAGTGACGGGAAAGAGATCAAAAAGG

1. SEQ05_ORF [1596]
860 AAG | 870 880 890 AA | 900
T-TCTGCTGTAGAAAAAGAGGATTTCGTATTCAATTTCAAAGATCTGAA>
| | || | ||| | || | || | ||| || | |

AF121782 TCTTTGATTTAGAGACAGTTGTCAATCACTGCCCTTTCTCTAGTTTTTCC

AF121782 45160 45170 45180 45190 45200
ATATACATGACTATATTTCTCTGCTTGCATCATTTATCAACTCTGAAGCA
TATATGTACTGATATAAAGAGACGAACGTAGTAAATAGTTGAGACTTCGT

1. SEQ05_ORF [1596]
910 920 930 940 950
AAAGAGAAGAC-AAACAAAGAAAC-TGAGACAGAAAGTGGAAATGAAAAC>
| | | | ||| | | | || | || | | |||

AF121782 ATATACATGACTATATTTCTCTGCTTGCATCATTTATCAACTCTGAAGCA

45460 45470 45480 45490 45500
AF121782 TAGTCTTACCAAAATTTAATCACTTTGCATTCTTTAAAAGTGTATTTATA
ATCAGAATGGTTTTAAATTAGTGAAACGTAAGAAATTTTCACATAAATAT